

**Amendments to the claims:**

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a substantially purified AvVIII peptide with cellulase activity and, ~~said AvVIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme having at least 70 90% identity to SEQ ID NO. 1, said AvVIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.~~, ~~the catalytic domain GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvVIII\_Aac):~~

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GH74_Ace ----- NFEQPYTWENVAICGGG-FVDCIVFNECAPGILYVATDICCNYRWDAAACNRWIPLLDHWG
AvVIII_Aac ----- AASQAYTNKAFATCGCGGCTPGIVFNPBAKGVAYARTDCCAYRLNDD TWTPLMDHWG
* * * * *

GH74_Ace ----- WRTWGYKGVGCIADDPINTNKKAAVGMVTSNDDPNDGAILRSGDQCATNQITPLDFKLC
AvVIII_Aac ----- NOTMHDWGDALATDPVDTDRVFAVGMVTSNDDPNDGAILRSGDQCATNQITPLDFKLC
* * * * *

GH74_Ace ----- GNMPCRCMGERLAVDPNNKNSILYFCARSGHGLWKSTDYCATWGNVTSFTNTGTYFQDSSS
AvVIII_Aac ----- GNMPCRCMGERLAVDPNNKNSILYFCARSGHGLWKSTDYCATWGNVTSFTNTGTYFQDSSS
* * * * *

GH74_Ace ----- TFCYQSDIQGVAAWAFDKSSSLQQAQKTIFFGVADPNNPVFWSRDGCATWQAVPGAP T
AvVIII_Aac ----- T YTESPVGIAWVTFDSTSGSGGATPRIFFGVADACKGVFKCEDAGATWAVSGEPQV
* * * * *

GH74_Ace ----- GPIDHKGVFDVWHPVLYIATGNTCCPVDGSGCDVWKPSVTSGTNRIGPVPDGTDTANDVP
AvVIII_Aac ----- CFLPHKGVLSPEEKTLYIEXANGAGPYDGTNCTVHKNTISGVNTDISP TSLASTPY
* * * * *

GH74_Ace ----- GYGGLTIDRQHTNTINVATQIGNWPDTIIFRSTDCGATWTRINWBTGYPNRGLRIVLDIG
AvVIII_Aac ----- GYGGLTIDRQHTNTINVATQIGNWPDTIIFRSTDCGATWTRINWBTGYPNRGLRIVLDIG
* * * * *

GH74_Ace ----- AEPWLTFCVQHNFPVTSFKLGMDEAMAIDPFNSDRMLYGTGATLYATNDLTWDSGGQI
AvVIII_Aac ----- NAPWIDTITSTDDFP VRVGMNVEALAIIDPFNSDRMLYGTGATLYATNDLTWDSGGQI
* * * * *

GH74_Ace ----- HIAPNVKLEETAVNDLISPPCCAPLICGLGCGFFHADVTAVPSTIFTCPVFTTCTCV
AvVIII_Aac ----- TVKSLAVGIBHAWGLITPPGAPALDVRVSDGCGFFHADVTAVPSTIFTCTCAVLCADGDT
* * * * *

GH74_Ace ----- DYAEINPSTIVRAGCTDPGCGQVDRHVAFTDGGKMTFQGGGCVTTGCTVAACAGCCR
AvVIII_Aac ----- DYAGNKPENIVRGCASDDYT TLALCGNFGCTVPRDYAGCTGTCTCAVLCADGDT
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GH74_Acc-----TUNADGDDGQDVVAVAVGRCNGWAAGGVPAAGIISGRVNFKTFYALENGTFYRSTDCGV
AviIII_Acc-----VLENGSTGALVSKGQG-----TLAVGSLPSCAVIASDESDNTVPTGGGAGATTFVCIQTAT
-----
GH74_Acc-----TFQDVNAGLPSSGAVGVMPHNAVCKESCDLWLAASSGLVHSTNGGCGWCAI-----TGVCANAV
AviIII_Acc-----GPTKTVG LGSETTFVNAIR AHPSTACDVNASTDKCLWHSTDVGSTFTQIGSGVTAGWGF
-----
GH74_Acc-----CPCKSAFCSSVPAVPAVGTIGGVFGAVRSDDEGFTFWLINDBQHQYEN WCAITCEKIAN
AviIII_Acc-----CPCKASSTCGVPAVIVCFETIEDCANGLPRGSDAGTINWQVICDAGHGFCCGCAVFWNGDLQT
-----
GH74_Acc-----LRRVVICTNVRGRTIVYEDIGGAPSG
AviIII_Acc-----YGRVFRGHRPCHLLRGGGREFPAG
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2. (Previously Presented) The composition of claim 1 wherein the AviIII peptide is further defined as comprising a linker and a signal sequence.
3. (Cancelled)
4. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.
5. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 90 amino acids.
6. (Previously Presented) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.
7. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.
8. (Previously Presented) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.
9. (Previously Presented) The composition of claim 1 wherein said AviIII protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74\_Ace has at least 90% sequence identity with SEQ ID NO: 3.

11. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.

12. (Previously Presented) An isolated AvIII peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Previously Presented) An industrial mixture suitable for degrading cellulose, such mixture comprising the AvIII polypeptide of claim 1.

15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[.]

16-27 (Cancelled)

28. (Previously Presented) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;
- c) a polypeptide sequence of SEQ ID NO: 5;
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.



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GH74_Ace      TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNEVPFWSRDGGATWQAVPGAP-T
AviIII_Aac    T--YTSDFVGIWVTFDSTSGSSGSGATPRIFVGVADAGKSVFKSEDAGATWAWVSGBPQY
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GH74_Ace      GFIPHKGVDFVNMVLYIATSTNGQPYDGSSEGDVWKFVSUTSGTWIRISFVPSSTDANDYF
AviIII_Aac    GFLPHKGVLSPKTKLYISYANGAGPYDGTNGTVHKYNITSGVWTDISP---TSLASTYY
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GH74_Ace      GYSGLTIDROHPNTIMVATQISWNPDTIIFRSTDGGATWTRIWDNTSYPNRSIRYVLDIS
AviIII_Aac    OYGGLSVDLQVPGITLMVAALNCWPFDELIFRSTDGATWSPINWNGYPSINYYSYDIS
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GH74_Ace      AEPWLTFGVQFNPPVPSKLGWMEAMAIDPFNSDRMLYGTGATLYATNDLTQWDSGGQI
AviIII_Aac    NAFWIQDTTSTDQFF--VRVGWVVEALAIIDPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GH74_Ace      HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSVPFTTGTSV
AviIII_Aac    TVKSLAVGIEEMAVLGLITPPGCGFALLSAVGDDGGFYHSDLDAAPNQAYHTPTPYGTINGI
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GH74_Ace      DYAEINPSIIVRAGSFDPSSQPNDRHVAFTDGGKMWFGQSEPGGVTTGGTVAASADGSR
AviIII_Aac    DYAGNKFSNIVRSGASDDYP-----TLALSNNFGSTWYADYAASTSTGTGAVALSADGDT
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GH74_Ace      FVWAPGDPGQPVVYAVGFGNSWAASQGVFANAQIRSDRVNPKTFYALSNGTFYRSTDGGV
AviIII_Aac    VLLMSSTSGALVSKSQG---TLTAVSSSLPSGAVIASDKSDNTVYFGGSAGAIYVSKNTAT
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GH74_Ace      TFQFVAAGLPSSGAVGVMPHAFVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII_Aac    SPTKTVS-LGSSSTIVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGNSF
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GH74_Ace      GFGKSAPGSSYPVAVFVGTIGGVGTGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac    GPGKASSTGSYVVYVYGFPTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVGDLQT
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GH74_Ace      LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac    YGRVFRGHERPGHLLRQSREPAG
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51. (New) The composition of claim 50 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

52. (New) A composition comprising a substantially purified AviIII peptide having an amino acid sequence identical to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.

53. (New) A composition comprising a substantially purified AviIII peptide, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain GH74\_Ace having a sequence that is at least 90% identical to SEQ ID NO. 3.

54. (New) The composition of claim 51 wherein said catalytic domain GH74\_Ace has a sequence identical to SEQ ID NO. 3.